

## AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-13. (canceled)

14. (currently amended) A method for the ~~enzymatic~~ production of L-amino acids ~~in~~ using coryneform bacteria comprising:

a) fermenting, ~~in a medium,~~ the coryneform bacteria which produce the a desired L-amino acid ~~and in which at least the sigC gene or nucleotide sequences coding for the latter are enhanced~~ comprising an overexpressed polynucleotide sigC wherein said polynucleotide comprises a nucleotide sequence of SEQ ID NO:1 and encodes a polypeptide having an RNA polymerase sigma-C factor activity.

15. (canceled)

16. (currently amended) The method according to claim ~~15~~ 14, further comprising:

e) isolating the L-amino acid.

17. (currently amended) The method according to claim 14, wherein the L amino acids are ~~acid is~~ lysine.

18. (currently amended) ~~The method according to claim 14, wherein coryneform bacteria in which at least the sigC gene or nucleotide sequences coding for the latter are~~

overexpressed are fermented A method for the production of L-amino acids using coryneform bacteria comprising:  
fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:2.

19-20. (canceled)

21. (original) The method according to claim 14, wherein a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigC gene.

22-24. (canceled)

25. (currently amended) The method according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced overexpressed; wherein the one or more genes is/are selected from the group consisting of:

the gene dapA coding for dihydrodipicolinate synthase,  
the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,  
the gene tpi coding for triosephosphate isomerase,  
the gene pgk coding for 3-phosphoglycerate kinase,  
the gene zwf coding for glucose-6-phosphate dehydrogenase,  
the gene pyc coding for pyruvate carboxylase,  
the gene mqo coding for malate-quinone-oxidoreductase,

the gene lysC coding for a feedback-resistant aspartate kinase,  
the gene lysE coding for a protein for lysine export,  
the gene hom coding for homoserine dehydrogenase,  
the gene ilvA coding for threonine dehydratase or the allele ilvA(Fbr) coding  
for a feedback-resistant threonine dehydratase,  
the gene ilvBN coding for acetohydroxy acid synthase,  
the gene ilvD coding for dihydroxy acid dehydratase, and  
the gene zwal coding for the Zwal protein.

26. Process according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated eliminated; wherein the genes are selected from the group consisting of:  
the gene pck coding for phosphoenol pyruvate carboxykinase,  
the gene pgi coding for glucose-6-phosphate isomerase,  
the gene poxB coding for pyruvate oxidase, and  
the gene zwa2 coding for the Zwa2 protein.
27. (currently amended) The method according to claim 14 wherein microorganisms the bacteria of the genus is Corynebacterium glutamicum are used.
28. (currently amended) The method according to claim 27, wherein the Corynebacterium glutamicum is a strain of DH5 $\alpha$ mcr/pEC-XK99EsigCb2ex is used.
29. (currently amended) The method according to claim 27, wherein the Corynebacterium glutamicum is a strain of DSM5715/pEC-XK99E is used.
- 30-32. (canceled)